AMENDMENT

In the Specification:

Following the abstract, please insert the enclosed Substitute Sheets as replacement pages 1 through 3 of the Sequence Listing submitted previously for the above-referenced patent application.

Please amend the specification as follows:

Paragraph 0021 has been amended as follows:

[0021] An RNA of the present invention may have a foreign gene inserted into an appropriate site. To express a desired protein, a foreign gene encoding the protein is inserted. In the case of Sendai virus RNA (GenBank accession No. M30202), a sequence with a multiple of six bases between the R1 and R2 sequences (J. Virol., Vol. 67, No. 8, 1993, 4822-4830) is inserted. The consensus sequences of R1 and R2 are 5'-AGGGWBAAWGD-3' (SEQ ID NO:5) and 5'-DTAAGAAAAA-3' (SEQ ID NO:6), respectively. The expression level of the inserted foreign gene can be regulated by the inserted position or the RNA nucleotide sequences flanking the inserted gene. For example, for Sendai virus RNA, it is known that the expression level of the inserted gene is higher as the insert position is nearer to the NP gene.

Paragraph 0030 has been amended as follows:

[0030] Figure 2 (SEQ ID NO:7) schematically shows the region carrying the M gene in Sendai virus cDNA and procedure for subcloning or mutating the region. In the figure, E stands for transcription termination sequence; I, intervening sequence; and S, transcription initiation sequence. Boxes indicate the restriction sites used for the plasmid construction.

Paragraph 0031 has been amended as follows:

[0030] Figure 3 schematically shows procedures for introducing mutation to the M gene region of Sendai virus cDNA. The upper panel of A shows the structure of the Sendai virus

genome with each position of the NP, P(P/C), M, F, HN, and L genes. Lower panel shows the structure of the M gene, restriction sites, and positions of primers M1 and M2 used for the construction of the M defect type. B and C schematically show the construction of the M defect type and the M deletion type, respectively. Crossed out restriction sites indicate that they are mutated to be indigestible by the enzymes. D shows a comparison between the M defect and wild type M (SEQ ID NOS 8 and 9) genes in terms of both nucleotide and amino acid sequences. Dots in the M defect sequences mean that bases or amino acids are identical to the corresponding wild type sequences. "Ter" indicates a termination codon. Numerals indicate the base/amino acid position in the M gene sequence. E shows EA linker (SEQ ID NOS 1 and 2).